

SEQUENCE LISTING

<110> YOKOYAMA, KEIICHI
NAKAMURA, NAMI
MIWA, TETSUYA
SEGURO, KATSUYA

<120> PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE

<130> 0010-0937-0

<140> 09/109,063

<141> 1998-07-02

<150> JP 180010/1997

<151> 1997-07-04

<160> 62

<170> PatentIn Ver. 2.0

<210> 1

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial
Sequence:TRANSGLUTAMINASE

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Pro	Asp	Pro	Tyr	Arg	Pro	Ser	Tyr	Gly	Arg	Ala	Glu	Thr	Val	Val	Asn
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Asn	Tyr	Ile	Arg	Lys	Trp	Gln	Gln	Val	Tyr	Ser	His	Arg	Asp	Gly	Arg
	35					40						45			
Lys	Gln	Gln	Met	Thr	Glu	Glu	Gln	Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys
	50					55					60				
Val	Gly	Val	Thr	Trp	Val	Asn	Ser	Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu
	65				70				75						80
Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp	Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn
			85						90					95	
Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr	Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val
		100						105					110		
Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu	Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu
		115					120					125			

Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser
 130 135 140
 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala
 145 150 155 160
 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn
 165 170 175
 Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg
 180 185 190
 Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg
 195 200 205
 Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg
 210 215 220
 Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile
 225 230 235 240
 Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr
 245 250 255
 Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp
 260 265 270
 Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met
 275 280 285
 His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp
 290 295 300
 Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn
 305 310 315 320
 Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
 325 330

<210> 2
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<220>
 <221> CDS
 <222> (1)..(993)
 <223> IDENTIFICATION METHOD: S

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cca Pro	gat Asp	cca Pro	tat Tyr 20	cgt Arg	cca Pro	tct Ser	tat Tyr	ggt Gly 25	cgt Arg	gct Ala	gaa Glu	act Thr	gtt Val 30	gtt Val	aat Asn	96		
aat Asn	tat Tyr	att Ile 35	cgt Arg	aaa Lys	tgg Trp	caa Gln	caa Gln 40	gtt Val	tat Tyr	tct Ser	cat His	cgt Arg 45	gat Asp	ggt Gly	cgt Arg	144		
aaa Lys	caa Gln 50	caa Gln	atg Met	act Thr	gaa Glu	gaa Glu 55	caa Gln	cgt Arg	gaa Glu	tgg Trp	ctg Leu 60	tct Ser	tat Tyr	ggt Gly	tgc Cys	192		
gtt Val 65	ggt Gly	gtt Val	act Thr	tgg Trp	gtt Val 70	aac Asn	tct Ser	ggt Gly	cag Gln	tat Tyr 75	ccg Pro	act Thr	aac Asn	cgt Arg	ctg Leu 80	240		
gca Ala	ttc Phe	gct Ala	tcc Ser	ttc Phe 85	gat Asp	gaa Glu	gat Asp	cgt Arg	ttc Phe 90	aag Lys	aac Asn	gaa Glu	ctg Leu	aag Lys 95	aac Asn	288		
ggt Gly	cgt Arg	ccg Pro	cgt Arg 100	tct Ser	ggt Gly	gaa Glu	act Thr	cgt Arg 105	gct Ala	gaa Glu	ttc Phe	gaa Glu	ggt Gly 110	cgt Arg	gtt Val	336		
gct Ala	aag Lys	gaa Glu 115	tcc Ser	ttc Phe	gat Asp	gaa Glu	gag Glu 120	aaa Lys	ggc Gly	ttc Phe	cag Gln	cgt Arg 125	gct Ala	cgt Arg	gaa Glu	384		
gtt Val 130	gct Ala	tct Ser	gtt Val	atg Met	aac Asn	cgt Arg 135	gct Ala	cta Leu	gag Glu	aac Asn	gct Ala 140	cat His	gat Asp	gaa Glu	tct Ser	432		
gct Ala 145	tac Tyr	ctg Leu	gat Asp	aac Asn	ctg Leu 150	aag Lys	aag Lys	gaa Glu	ctg Leu	gct Ala 155	aac Asn	ggt Gly	aac Asn	gat Asp	gct Ala 160	480		
ctg Leu	cgt Arg	aac Asn	gaa Glu	gat Asp 165	gct Ala	cgt Arg	tct Ser	ccg Pro	ttc Phe 170	tac Tyr	tct Ser	gct Ala	ctg Leu	cgt Arg 175	aac Asn	528		
act Thr	ccg Pro	tcc Ser	ttc Phe 180	aaa Lys	gaa Glu	cgt Arg	aac Asn	ggt Gly 185	ggt Gly	aac Asn	cat His	gat Asp	ccg Pro 190	tct Ser	cgt Arg	576		
atg Met	aaa Lys	gct Ala 195	gtt Val	atc Ile	tac Tyr	tct Ser	aaa Lys 200	cat His	ttc Phe	tgg Trp	tct Ser	ggt Gly 205	cag Gln	gat Asp	aga Arg	624		
tct Ser	tct Ser 210	tct Ser	gct Ala	gat Asp	aaa Lys	cgt Arg 215	aaa Lys	tac Tyr	ggt Gly	gat Asp	ccg Pro 220	gat Asp	gca Ala	ttc Phe	cgt Arg	672		
ccg Pro	gct Ala	ccg Pro	ggt Gly	act Thr	ggt Gly	ctg Leu	gta Val	gac Asp	atg Met	tct Ser	cgt Arg	gat Asp	cgt Arg	aac Asn	atc Ile	720		

225	230	235	240	
ccg cgt tct ccg act tct ccg ggt gaa ggc ttc gtt aac ttc gat tac	768			
Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr				
245 250 255				
ggt tgg ttc ggt gct cag act gaa gct gat gct gat aag act gta tgg	816			
Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp				
260 265 270				
acc cat ggt aac cat tac cat gct ccg aac ggt tct ctg ggt gct atg	864			
Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met				
275 280 285				
cat gta tac gaa tct aaa ttc cgt aac tgg tct gaa ggt tac tct gac	912			
His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp				
290 295 300				
ttc gat cgt ggt gct tac gtt atc acc ttc att ccg aaa tct tgg aac	960			
Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn				
305 310 315 320				
act gct ccg gac aaa gtt aaa cag ggt tgg ccg	993			
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<211> 1519

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:SYNTHETIC DNA

<220>

<221> CDS

<222> (87)..(1082)

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Met Asp Ser Asp Asp Arg Val Thr Pro	
1 5	

cca gct gaa cca ctg gat cgt atg cca gat cca tat cgt cca tct tat	161
Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr	
10 15 20 25	

ggt cgt gct gaa act gtt gtt aat aat tat att cgt aaa tgg caa caa	209
Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln	
30 35 40	

ggt tat tct cat cgt gat ggt cgt aaa caa caa atg act gaa gaa caa	257
Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln	

45						50						55						
cgt	gaa	tgg	ctg	tct	tat	ggt	tgc	gtt	ggt	gtt	act	tgg	gtt	aac	tct	305		
Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys	Val	Gly	Val	Thr	Trp	Val	Asn	Ser			
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ggt	cag	tat	ccg	act	aac	cgt	ctg	gca	ttc	gct	tcc	ttc	gat	gaa	gat	353		
Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu	Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp			
	75					80					85							
cgt	ttc	aag	aac	gaa	ctg	aag	aac	ggt	cgt	ccg	cgt	tct	ggt	gaa	act	401		
Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn	Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr			
	90				95					100					105			
cgt	gct	gaa	ttc	gaa	ggt	cgt	gtt	gct	aag	gaa	tcc	ttc	gat	gaa	gag	449		
Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val	Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu			
				110					115					120				
aaa	ggc	ttc	cag	cgt	gct	cgt	gaa	gtt	gct	tct	gtt	atg	aac	cgt	gct	497		
Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu	Val	Ala	Ser	Val	Met	Asn	Arg	Ala			
			125					130					135					
cta	gag	aac	gct	cat	gat	gaa	tct	gct	tac	ctg	gat	aac	ctg	aag	aag	545		
Leu	Glu	Asn	Ala	His	Asp	Glu	Ser	Ala	Tyr	Leu	Asp	Asn	Leu	Lys	Lys			
		140					145					150						
gaa	ctg	gct	aac	ggt	aac	gat	gct	ctg	cgt	aac	gaa	gat	gct	cgt	tct	593		
Glu	Leu	Ala	Asn	Gly	Asn	Asp	Ala	Leu	Arg	Asn	Glu	Asp	Ala	Arg	Ser			
	155					160					165							
ccg	ttc	tac	tct	gct	ctg	cgt	aac	act	ccg	tcc	ttc	aaa	gaa	cgt	aac	641		
Pro	Phe	Tyr	Ser	Ala	Leu	Arg	Asn	Thr	Pro	Ser	Phe	Lys	Glu	Arg	Asn			
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Gly	Gly	Asn	His	Asp	Pro	Ser	Arg	Met	Lys	Ala	Val	Ile	Tyr	Ser	Lys			
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cat	ttc	tgg	tct	ggt	cag	gat	aga	tct	tct	tct	gct	gat	aaa	cgt	aaa	737		
His	Phe	Trp	Ser	Gly	Gln	Asp	Arg	Ser	Ser	Ser	Ala	Asp	Lys	Arg	Lys			
			205					210					215					
tac	ggt	gat	ccg	gat	gca	ttc	cgt	ccg	gct	ccg	ggt	act	ggt	ctg	gta	785		
Tyr	Gly	Asp	Pro	Asp	Ala	Phe	Arg	Pro	Ala	Pro	Gly	Thr	Gly	Leu	Val			
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gac	atg	tct	cgt	gat	cgt	aac	atc	ccg	cgt	tct	ccg	act	tct	ccg	ggt	833		
Asp	Met	Ser	Arg	Asp	Arg	Asn	Ile	Pro	Arg	Ser	Pro	Thr	Ser	Pro	Gly			
	235					240					245							
gaa	ggc	ttc	gtt	aac	ttc	gat	tac	ggt	tgg	ttc	ggt	gct	cag	act	gaa	881		
Glu	Gly	Phe	Val	Asn	Phe	Asp	Tyr	Gly	Trp	Phe	Gly	Ala	Gln	Thr	Glu			
	250				255					260					265			
gct	gat	gct	gat	aag	act	gta	tgg	acc	cat	ggt	aac	cat	tac	cat	gct	929		
Ala	Asp	Ala	Asp	Lys	Thr	Val	Trp	Thr	His	Gly	Asn	His	Tyr	His	Ala			

270

275

280

ccg aac ggt tct ctg ggt gct atg cat gta tac gaa tct aaa ttc cgt 977
 Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg
 285 290 295

aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc 1025
 Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile
 300 305 310

acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag 1073
 Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln
 315 320 325

ggt tgg ccg taatgaaagc ttggatctct aattactgga cttcacacag 1122
 Gly Trp Pro
 330

actaagatag acatatctta tattatgtga ttttgtgaca tttcctagat gtgaggtgga 1182
 ggtgatgtat aaggtagatg atgacacctt acgccggacg catcgtggcc ggcacaccg 1242
 gcgccacagg tgcggttgct ggcgcctata tcgccgacat caccgatggg gaagatcggg 1302
 ctcgcactt cgggctcatg agcgcttggt tcggcgtggg tatggtggca ggccccgtgg 1362
 ccgggggact gttggggcgcc atctccttgc atgcaccatt ccttgccggcg gcggtgctca 1422
 acggcctcaa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcgtc 1482
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<210> 4
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 4
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<210> 5
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 <212> DNA
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 5
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<210> 6
<211> 41
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 6
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41

<210> 7
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 7
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<210> 8
<211> 41
<212> DNA
<213> Artificial Sequence

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<400> 8
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41

<210> 9
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:SYNTHETIC DNA

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<210> 10
<211> 41
<212> DNA
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<400> 10
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<210> 11
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<400> 11
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<210> 12
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<400> 12
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<210> 13
 <211> 41
 <212> DNA
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<220>
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<400> 13
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<210> 14
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<220>
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<210> 15
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 15
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 <210> 16
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 <210> 17
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 <400> 17
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 <210> 18
 <211> 49
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 18
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 <210> 19
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 19
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 <210> 20

<211> 35
 <212> DNA
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 20
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 <210> 21
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 <212> DNA
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

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 <210> 22
 <211> 48
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 22
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 <210> 23
 <211> 48
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 23
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 <210> 24
 <211> 42
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 24

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<210> 25

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<212> DNA

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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 25

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<210> 26

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:SYNTHETIC DNA

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<210> 27

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<212> DNA

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<223> Description of Artificial Sequence:SYNTHETIC DNA

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<210> 28

<211> 49

<212> DNA

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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 28

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<210> 29

<211> 49

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

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 <210> 30
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 30
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 <210> 31
 <211> 39
 <212> DNA
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 31
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 <210> 32
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 32
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 <210> 33
 <211> 47
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 33
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 <210> 34

<211> 45
 <212> DNA
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 34
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 <210> 35
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 35
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 <210> 36
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

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 <210> 37
 <211> 44
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 37
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 <210> 38
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

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<210> 39
 <211> 48
 <212> DNA
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<220>
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<400> 39
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<210> 40
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 <212> DNA
 <213> Artificial Sequence

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<400> 40
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<210> 41
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<400> 41
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<210> 42
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 <212> DNA
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<220>
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<400> 42
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<210> 43
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 43
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 <220>
 <223> Description of Artificial Sequence:SYNTHETIC DNA

 <400> 44
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 <210> 45
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 <400> 45
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 <210> 46
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 <212> DNA
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 <400> 46
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 <210> 47
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<223> Description of Artificial Sequence:SYNTHETIC DNA

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<210> 56

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 <400> 61
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[illegible]